

WE CLAIM:

1. A method of detecting an ovarian cancer-associated transcript in a biological sample, the method comprising contacting the biological sample with a polynucleotide
5 that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Table 1 or 2 or 3.
2. A method of diagnosing an ovarian cancer in a human or animal subject being tested said method comprising contacting a biological sample from said subject being
10 tested with a nucleic acid probe for a time and under conditions sufficient for hybridization to occur and then detecting the hybridization wherein a modified level of hybridization of the probe for the subject being tested compared to the hybridization obtained for a control subject not having ovarian cancer indicates that the subject being tested has an ovarian cancer, and wherein said nucleic acid probe comprises a
15 sequence selected from the group consisting of:
 - (i) a sequence comprising at least about 20 contiguous nucleotides from a sequence selected from the group consisting of SEQ ID NOs: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 46, 48, 50, 52, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81 and 83;
 - 20 (ii) a sequence that hybridizes under at least low stringency hybridization conditions to at least about 20 contiguous nucleotides from a sequence selected from the group consisting of SEQ ID NOs: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 46, 48, 50, 52, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81 and 83;
 - 25 (iii) a sequence that is at least about 80% identical to a sequence selected from the group consisting of SEQ ID NOs: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 46, 48, 50, 52, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81 and 83;
 - (iv) a sequence that encodes an amino acid sequence selected from the group consisting of SEQ ID NOs: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 47, 49, 51, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82 and 84; and
 - 30 (v) a sequence that is complementary to any one of the sequences set forth in (i) or (ii) or (iii) or (iv).

3. A method of diagnosing an ovarian cancer in a human or animal subject being tested said method comprising contacting a biological sample from said subject being tested with a nucleic acid probe for a time and under conditions sufficient for hybridization to occur and then detecting the hybridization wherein a modified level of hybridization of the probe for the subject being tested compared to the hybridization obtained for a control subject not having ovarian cancer indicates that the subject being tested has an ovarian cancer, and wherein said nucleic acid probe comprises a sequence selected from the group consisting of:

- (i) a sequence comprising at least about 20 contiguous nucleotides from a sequence selected from the group consisting of SEQ ID NOs: 1, 5, 7, 9, 11, 13, 15, 17, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 45, 46, 48, 52, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81 and 83;
- (ii) a sequence that hybridizes under at least low stringency hybridization conditions to at least about 20 contiguous nucleotides from a sequence selected from the group consisting of SEQ ID NOs: 1, 5, 7, 9, 11, 13, 15, 17, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 45, 46, 48, 52, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81 and 83;
- (iii) a sequence that is at least about 80% identical to a sequence selected from the group consisting of SEQ ID NOs: 1, 5, 7, 9, 11, 13, 15, 17, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 45, 46, 48, 52, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81 and 83;
- (iv) a sequence that encodes an amino acid sequence selected from the group consisting of SEQ ID NOs: 2, 6, 8, 10, 12, 14, 16, 18, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 47, 49, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82 and 84; and
- (v) a sequence that is complementary to (i) or (ii) or (iii) or (iv).

4. The method of claim 2 or 3 wherein the hybridization is enhanced in the sample from the subject being tested compared to the hybridization obtained for a sample from a control subject not having ovarian cancer.

5. The method of claim 2 or 3 wherein the hybridization is reduced in the sample from the subject being tested compared to the hybridization obtained for a sample from a control subject not having ovarian cancer.

6. A method of diagnosing an ovarian cancer in a human or animal subject being tested said method comprising contacting a biological sample from said subject being tested with a nucleic acid probe for a time and under conditions sufficient for hybridization to occur and then detecting the hybridization wherein an enhanced level of hybridization of the probe for the subject being tested compared to the hybridization obtained for a control subject not having ovarian cancer indicates that the subject being tested has an ovarian ovarian cancer, and wherein said nucleic acid probe comprises a sequence selected from the group consisting of:

- (i) a sequence comprising at least about 20 contiguous nucleotides from a nucleic acid set forth in Table 1 or 2 other than a nucleic acid having an Accession Number selected from the group consisting of NM_022117, NM_005460, NM_002387, AI745249 and AI694200;
- (ii) a sequence that hybridizes under at least low stringency hybridization conditions to at least about 20 contiguous nucleotides from a nucleic acid set forth in Table 1 or 2 other than a nucleic acid having an Accession Number selected from the group consisting of NM_022117, NM_005460, NM_002387, AI745249 and AI694200;
- (iii) a sequence that is at least about 80% identical to (i) or (ii);
- (iv) a sequence that encodes a polypeptide encoded by a nucleic acid set forth in Table 1 or 2 other than a nucleic acid having an Accession Number selected from the group consisting of NM_022117, NM_005460, NM_002387, AI745249 and AI694200; and
- (v) a sequence that is complementary to any one of the sequences set forth in (i) or (ii) or (iii) or (iv).

7. The method of claim 6 wherein the nucleic acid probe comprises a sequence selected from the group consisting of:

- (i) a sequence comprising at least about 20 contiguous nucleotides from a sequence selected from the group consisting of SEQ ID NOs: 7, 9, 11, 13, 15, 17, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 45, 46, 48, 52, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81 and 83;
- (ii) a sequence that hybridizes under at least low stringency hybridization conditions to at least about 20 contiguous nucleotides from a sequence selected from the group consisting of SEQ ID NOs: 7, 9, 11, 13, 15, 17, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 45, 46, 48, 52, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81 and 83;

- (iii) a sequence that is at least about 80% identical to a sequence selected from the group consisting of SEQ ID NOs: 7, 9, 11, 13, 15, 17, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 45, 46, 48, 52, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81 and 83;
- 5 (iv) a sequence that encodes an amino acid sequence selected from the group consisting of SEQ ID NOs: 8, 10, 12, 14, 16, 18, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 47, 49, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82 and 84; and
- (v) a sequence that is complementary to any one of the sequences set forth in (i) or
10 (ii) or (iii) or (iv).

8. A method of diagnosing an ovarian cancer in a human or animal subject being tested said method comprising contacting a biological sample from said subject being tested with a nucleic acid probe for a time and under conditions sufficient for
15 hybridization to occur and then detecting the hybridization wherein a reduced level of hybridization of the probe for the subject being tested compared to the hybridization obtained for a control subject not having ovarian cancer indicates that the subject being tested has an ovarian ovarian cancer, and wherein said nucleic acid probe comprises a sequence selected from the group consisting of:

- 20 (i) a sequence comprising at least about 20 contiguous nucleotides from a nucleic acid set forth in Table 1 and having an Accession Number selected from the group consisting of NM_022117, NM_005460, NM_002387, AI745249 and AI694200;
- (ii) a sequence that hybridizes under at least low stringency hybridization conditions to at least about 20 contiguous nucleotides from a nucleic acid set forth in Table 1
25 and having an Accession Number selected from the group consisting of NM_022117, NM_005460, NM_002387, AI745249 and AI694200;
- (iii) a sequence that is at least about 80% identical to (i) or (ii);
- (iv) a sequence that encodes a polypeptide encoded by a nucleic acid set forth in Table 1 and having an Accession Number selected from the group consisting of
30 NM_022117, NM_005460, NM_002387, AI745249 and AI694200; and
- (v) a sequence that is complementary to any one of the sequences set forth in (i) or (ii) or (iii) or (iv).

9. The method of claim 8 wherein the nucleic acid probe comprises a sequence
35 selected from the group consisting of:

- (i) a sequence comprising at least about 20 contiguous nucleotides from a sequence selected from the group consisting of SEQ ID NOs: 1, 3, and 5;
- (ii) a sequence that hybridizes under at least low stringency hybridization conditions to at least about 20 contiguous nucleotides from a sequence selected from the group consisting of SEQ ID NOs: 1, 3, and 5;
- (iii) a sequence that is at least about 80% identical to a sequence selected from the group consisting of SEQ ID NOs: 1, 3, and 5;
- (iv) a sequence that encodes an amino acid sequence selected from the group consisting of SEQ ID NOs: 2, 4, and 6; and
- (v) a sequence that is complementary to any one of the sequences set forth in (i) or (ii) or (iii) or (iv).

10. The method according to any one of claims 1 to 9 wherein the ovarian cancer that is diagnosed is an epithelial ovarian cancer.

11. The method according to any one of claims 1 to 9 wherein the ovarian cancer that is diagnosed is selected from the group consisting of serous ovarian cancer, non-invasive ovarian cancer, mixed phenotype ovarian cancer, mucinous ovarian cancer, endometrioid ovarian cancer, clear cell ovarian cancer, papillary serous ovarian cancer, Brenner cell and undifferentiated adenocarcinoma.

12. The method according to claim 11 wherein the ovarian cancer that is diagnosed is selected from the group consisting of serous ovarian cancer, mucinous ovarian cancer, endometrioid ovarian cancer and clear cell ovarian cancer.

13. A method of diagnosing a serous ovarian cancer in a human or animal subject being tested said method comprising contacting a biological sample from said subject being tested with a nucleic acid probe for a time and under conditions sufficient for hybridization to occur and then detecting the hybridization wherein a modified level of hybridization of the probe for the subject being tested compared to the hybridization obtained for a control subject not having ovarian cancer indicates that the subject being tested has a serous ovarian cancer, and wherein said nucleic acid probe comprises a sequence selected from the group consisting of:

- (i) a sequence comprising at least about 20 contiguous nucleotides from a nucleic acid set forth in Table 2 or as set forth in Table 1 and having an Accession

Number selected from the group consisting of: U62801, D49441, X51630, And AB018305;

- (ii) a sequence that hybridizes under at least low stringency hybridization conditions to at least about 20 contiguous nucleotides from a nucleic acid set forth in Table 2 or as set forth in Table 1 and having an Accession Number selected from the group consisting of: U62801, D49441, X51630, And AB018305;
- (iii) a sequence that is at least about 80% identical to (i) or (ii);
- (iv) a sequence that encodes a polypeptide encoded by a nucleic acid set forth in Table 2 or as set forth in Table 1 and having an Accession Number selected from the group consisting of: U62801, D49441, X51630, And AB018305; and
- (v) a sequence that is complementary to any one of the sequences set forth in (i) or (ii) or (iii) or (iv).

14. A method of diagnosing a mucinous ovarian cancer in a human or animal subject being tested said method comprising contacting a biological sample from said subject being tested with a nucleic acid probe for a time and under conditions sufficient for hybridization to occur and then detecting the hybridization wherein an elevated level of hybridization of the probe for the subject being tested compared to the hybridization obtained for a control subject not having ovarian cancer indicates that the subject being tested has a mucinous ovarian cancer, and wherein said nucleic acid probe comprises a sequence selected from the group consisting of:

- (i) a sequence comprising at least about 20 contiguous nucleotides from a nucleic acid set forth in Table 1 and having an Accession Number selected from the group consisting of: NM_006149, AA315933, U47732, NM_005588, AW503395, NM_004063, AI073913, AI928445, NM_022454, W40460, AA132961 and AF111856;
- (ii) a sequence that hybridizes under at least low stringency hybridization conditions to at least about 20 contiguous nucleotides from a nucleic acid set forth in Table 1 and having an Accession Number selected from the group consisting of: NM_006149, AA315933, U47732, NM_005588, AW503395, NM_004063, AI073913, AI928445, NM_022454, W40460, AA132961 and AF111856;
- (iii) a sequence that is at least about 80% identical to (i) or (ii);
- (iv) a sequence that encodes a polypeptide encoded by a nucleic acid set forth in Table 1 and having an Accession Number selected from the group consisting of: NM_006149, AA315933, U47732, NM_005588, AW503395, NM_004063, AI073913, AI928445, NM_022454, W40460, AA132961 and AF111856; and

- (v) a sequence that is complementary to any one of the sequences set forth in (i) or (ii) or (iii) or (iv).

15. The method of claim 14 wherein the nucleic acid probe comprises a sequence
5 selected from the group consisting of:

- (i) a sequence comprising at least about 20 contiguous nucleotides from SEQ ID NO: 57 or 59 or 61;
(ii) a sequence that hybridizes under at least low stringency hybridization conditions to at least about 20 contiguous nucleotides from SEQ ID NO: 57 or 59 or 61;
10 (iii) a sequence that is at least about 80% identical to SEQ ID NO: 57 or 59 or 61;
(iv) a sequence that encodes the amino acid sequence set forth in SEQ ID NO: 58 or 60 or 62; and
(v) a sequence that is complementary to any one of the sequences set forth in (i) or (ii) or (iii) or (iv).

15 16. The method according to any one of claims 1 to 15 comprising performing a PCR reaction.

20 17. The method according to any one of claims 1 to 16 comprising performing a nucleic acid hybridization.

18. A method of detecting an ovarian cancer-associated polypeptide in a biological sample the method comprising contacting the biological sample with an antibody that binds specifically to an ovarian cancer-associated polypeptide in the biological sample,
25 the polypeptide being encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-3.

19. A method of diagnosing an ovarian cancer in a human or animal subject being tested said method comprising contacting a biological sample from said subject being
30 tested with an antibody for a time and under conditions sufficient for an antigen-antibody complex to form and then detecting the complex wherein a modified level of the antigen-antibody complex for the subject being tested compared to the amount of the antigen-antibody complex formed for a control subject not having ovarian cancer indicates that the subject being tested has an ovarian cancer, and wherein said antibody binds to a
35 polypeptide comprising an amino acid sequence comprising at least about 10 contiguous amino acid residues of a sequence having at least about 80% identity to a sequence

selected from the group consisting of SEQ ID NOs: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 47, 49, 51, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82 and 84.

5 20. The method of claim 19 wherein the antibody binds to a polypeptide comprising an amino acid sequence comprising at least about 10 contiguous amino acid residues of a sequence having at least about 80% identity to a sequence selected from the group consisting of SEQ ID NOs: 2, 6, 8, 10, 12, 14, 16, 18, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 47, 49, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82 and 84.

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21. A method of diagnosing an ovarian cancer in a human or animal subject being tested said method comprising contacting a biological sample from said subject being tested with an antibody for a time and under conditions sufficient for an antigen-antibody complex to form and then detecting the complex wherein an enhanced level of the
15 antigen-antibody complex for the subject being tested compared to the amount of the antigen-antibody complex formed for a control subject not having ovarian cancer indicates that the subject being tested has an ovarian cancer, and wherein said antibody binds to a polypeptide comprising an amino acid sequence comprising at least about 10 contiguous amino acid residues of a polypeptide encoded by a nucleic acid set forth in
20 Table 1 or 2 other than a nucleic acid having an Accession Number selected from the group consisting of NM_022117, NM_005460, NM_002387, AI745249 and AI694200.

22. The method of claim 21 wherein the antibody binds to a polypeptide comprising an amino acid sequence comprising at least about 10 contiguous amino acid residues of
25 a sequence having at least about 80% identity to a sequence selected from the group consisting of SEQ ID NOs: 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 47, 49, 51, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82 and 84.

23. A method of diagnosing an ovarian cancer in a human or animal subject being
30 tested said method comprising contacting a biological sample from said subject being tested with an antibody for a time and under conditions sufficient for an antigen-antibody complex to form and then detecting the complex wherein a reduced level of the antigen-antibody complex for the subject being tested compared to the amount of the antigen-antibody complex formed for a control subject not having ovarian cancer indicates that
35 the subject being tested has an ovarian cancer, and wherein said antibody binds to a polypeptide comprising an amino acid sequence comprising at least about 10 contiguous

amino acid residues of a polypeptide encoded by a nucleic acid set forth in Table 1 and having an Accession Number selected from the group consisting of NM_022117, NM_005460, NM_002387, AI745249 and AI694200.

- 5 24. The method of claim 23 wherein the antibody binds to a polypeptide comprising an amino acid sequence comprising at least about 10 contiguous amino acid residues of a sequence having at least about 80% identity to a sequence selected from the group consisting of SEQ ID NOs: 2, 4, and 6.
- 10 25. The method according to any one of claims 19 to 24 wherein the ovarian cancer that is diagnosed is an epithelial ovarian cancer.
- 15 26. The method according to any one of claims 19 to 24 wherein the ovarian cancer that is diagnosed is selected from the group consisting of serous ovarian cancer, non-invasive ovarian cancer, mixed phenotype ovarian cancer, mucinous ovarian cancer, endometrioid ovarian cancer, clear cell ovarian cancer, papillary serous ovarian cancer, Brenner cell and undifferentiated adenocarcinoma.
- 20 27. The method according to claim 26 wherein the ovarian cancer that is diagnosed is selected from the group consisting of serous ovarian cancer, mucinous ovarian cancer, endometrioid ovarian cancer and clear cell ovarian cancer.
- 25 28. A method of diagnosing a serous ovarian cancer in a human or animal subject being tested said method comprising contacting a biological sample from said subject being tested with an antibody for a time and under conditions sufficient for an antigen-antibody complex to form and then detecting the complex wherein a modified level of the antigen-antibody complex for the subject being tested compared to the amount of the antigen-antibody complex formed for a control subject not having ovarian cancer indicates that the subject being tested has a serous ovarian cancer, and wherein said
- 30 antibody binds to a polypeptide comprising an amino acid sequence comprising at least about 10 contiguous amino acid residues of a polypeptide encoded by a nucleic acid set forth in Table 2 or as set forth in Table 1 and having an Accession Number selected from the group consisting of: U62801, D49441, X51630, And AB018305.
- 35 29. A method of diagnosing a mucinous ovarian cancer in a human or animal subject being tested said method comprising contacting a biological sample from said subject

being tested with an antibody for a time and under conditions sufficient for an antigen-antibody complex to form and then detecting the complex wherein a reduced level of the antigen-antibody complex for the subject being tested compared to the amount of the antigen-antibody complex formed for a control subject not having ovarian cancer indicates that the subject being tested has a mucinous ovarian cancer, and wherein said antibody binds to a polypeptide comprising an amino acid sequence comprising at least about 10 contiguous amino acid residues of a polypeptide encoded by a nucleic acid set forth in Table 1 and having an Accession Number selected from the group consisting of: NM_006149, AA315933, U47732, NM_005588, AW503395, NM_004063, AI073913, AI928445, NM_022454, W40460, AA132961 and AF111856.

30. The method according to claim 29 wherein the antibody binds to a polypeptide comprising an amino acid sequence comprising at least about 10 contiguous amino acid residues of a sequence having at least about 80% identity to SEQ ID NO: 58 or 60 or 62.

31. A method of detecting an ovarian cancer-associated antibody in a biological sample the method comprising contacting the biological sample with a polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-3, wherein the polypeptide specifically binds to the ovarian cancer-associated antibody.

32. The method according to any one of claims 1 to 31 wherein the biological sample is contacted with a plurality of nucleic acid probes and/or antibodies and/or polypeptides.

33. The method according to any one of claims 1 to 32 wherein the subject being tested is a patient undergoing a therapeutic regimen to treat ovarian cancer.

34. The method according to any one of claims 1 to 32 wherein the subject being tested is a subject suspected of having ovarian cancer.

35. A method of monitoring the efficacy of a therapeutic treatment of ovarian cancer, the method comprising:

(i) providing a biological sample from a patient undergoing the therapeutic treatment; and

(ii) determining the level of a ovarian cancer-associated transcript in the biological sample by contacting the biological sample with a polynucleotide

that selectively hybridizes to a sequence having at least about 80% identity to a sequence as shown in any one of Tables 1-3, thereby monitoring the efficacy of the therapy.

- 5 36. The method according to claim 35 further comprising comparing the level of the ovarian cancer-associated transcript to a level of the ovarian cancer-associated transcript in a biological sample from the patient prior to, or earlier in, the therapeutic treatment.
- 10 37. A method of monitoring the efficacy of a therapeutic treatment of ovarian cancer, the method comprising :
- (i) providing a biological sample from a patient undergoing the therapeutic treatment; and
 - (ii) determining the level of a ovarian cancer-associated antibody in the biological sample by contacting the biological sample with a polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-3, wherein the polypeptide specifically binds to the ovarian cancer-associated antibody, thereby monitoring the efficacy of the therapy.
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- 20 38. The method of claim 37 further comprising comparing the level of the ovarian cancer-associated antibody to a level of the ovarian cancer-associated antibody in a biological sample from the patient prior to, or earlier in, the therapeutic treatment.
- 25 39. A method of monitoring the efficacy of a therapeutic treatment of ovarian cancer, the method comprising :
- (i) providing a biological sample from a patient undergoing the therapeutic treatment; and
 - (ii) determining the level of a ovarian cancer-associated polypeptide in the biological sample by contacting the biological sample with an antibody, wherein the antibody specifically binds to a polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-3, thereby monitoring the efficacy of the therapy.
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40. The method of claim 39 further comprising comparing the level of the ovarian cancer-associated polypeptide to a level of the ovarian cancer-associated polypeptide in a biological sample from the patient prior to, or earlier in, the therapeutic treatment.

5 41. The method according to any one of claims 35 to 40 wherein the ovarian cancer that is diagnosed is an epithelial ovarian cancer.

42. The method according to any one of claims 35 to 41 wherein the ovarian cancer that is diagnosed is selected from the group consisting of serous ovarian cancer, non-
10 invasive ovarian cancer, mixed phenotype ovarian cancer, mucinous ovarian cancer, endometrioid ovarian cancer, clear cell ovarian cancer, papillary serous ovarian cancer, Brenner cell and undifferentiated adenocarcinoma.

43. The method according to claim 42 wherein the ovarian cancer that is diagnosed is
15 selected from the group consisting of serous ovarian cancer, mucinous ovarian cancer, endometrioid ovarian cancer and clear cell ovarian cancer.

44. A method of determining the likelihood of survival of a subject suffering from an ovarian cancer, said method comprising contacting a biological sample from said subject
20 being tested with a nucleic acid probe for a time and under conditions sufficient for hybridization to occur and then detecting the hybridization wherein an elevated level of hybridization of the probe for the subject being tested compared to the hybridization obtained for a control subject not having ovarian cancer indicates that the subject being tested has a poor probability of survival, and wherein said nucleic acid probe comprises a
25 sequence selected from the group consisting of:

- (i) a sequence comprising at least about 20 contiguous nucleotides from a nucleic acid set forth in Table 1 and having an Accession Number selected from the group consisting of: NM_003014, AA046217, NM_015902, T83882, AB040888, AA628980, AI623351, AW614420, AA243499, AF251237, AI970797, AF145713, X78565, T97307, BE243845, AW068302, AL133561, BE313555, X07820, AI973016, AF084545, U41518, Z11894, AW138190, BE086548, W47196, AI796870, X02761, AW968613, AW972565, AF045229, AW953853, U52426, F06700, AI798863, H52761, BE546947, AU076643, U20536, AA581602, AJ245210, X65965, AI806770, BE386490, AW581992, U77534, AL034417, L10343, AW518944, W28729, AI640160, U11862, AW295980, X59135, BE466173, AI354722, M90464, AA829286, AI333771, BE465867, NM_014992,
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BE616902, AA430373, R27430, BE387335, AW264102, AW952323, AA088177, BE614567, AL079658, NM_002776, BE261944, NM_006379, AI002238, X81789, NM_002122, AB001914, AA311919, AI381750, AA292998, BE439580, AI677897, N72403, BE003054, AL035588, AI080491, AW770994, H24177, AF146761, NM_001955, AI680737, AI752666, AA505445, BE246649, and NM_003955;

- (ii) a sequence that hybridizes under at least low stringency hybridization conditions to at least about 20 contiguous nucleotides from a nucleic acid set forth in Table 1 and having an Accession Number selected from the group consisting of: NM_003014, AA046217, NM_015902, T83882, AB040888, AA628980, AI623351, AW614420, AA243499, AF251237, AI970797, AF145713, X78565, T97307, BE243845, AW068302, AL133561, BE313555, X07820, AI973016, AF084545, U41518, Z11894, AW138190, BE086548, W47196, AI796870, X02761, AW968613, AW972565, AF045229, AW953853, U52426, F06700, AI798863, H52761, BE546947, AU076643, U20536, AA581602, AJ245210, X65965, AI806770, BE386490, AW581992, U77534, AL034417, L10343, AW518944, W28729, AI640160, U11862, AW295980, X59135, BE466173, AI354722, M90464, AA829286, AI333771, BE465867, NM_014992, BE616902, AA430373, R27430, BE387335, AW264102, AW952323, AA088177, BE614567, AL079658, NM_002776, BE261944, NM_006379, AI002238, X81789, NM_002122, AB001914, AA311919, AI381750, AA292998, BE439580, AI677897, N72403, BE003054, AL035588, AI080491, AW770994, H24177, AF146761, NM_001955, AI680737, AI752666, AA505445, BE246649, and NM_003955;

- (iii) a sequence that is at least about 80% identical to (i) or (ii);

- (iv) a sequence that encodes a polypeptide encoded by a nucleic acid set forth in Table 1 and having an Accession Number selected from the group consisting of: NM_003014, AA046217, NM_015902, T83882, AB040888, AA628980, AI623351, AW614420, AA243499, AF251237, AI970797, AF145713, X78565, T97307, BE243845, AW068302, AL133561, BE313555, X07820, AI973016, AF084545, U41518, Z11894, AW138190, BE086548, W47196, AI796870, X02761, AW968613, AW972565, AF045229, AW953853, U52426, F06700, AI798863, H52761, BE546947, AU076643, U20536, AA581602, AJ245210, X65965, AI806770, BE386490, AW581992, U77534, AL034417, L10343, AW518944, W28729, AI640160, U11862, AW295980, X59135, BE466173, AI354722, M90464, AA829286, AI333771, BE465867, NM_014992, BE616902, AA430373, R27430, BE387335, AW264102, AW952323, AA088177, BE614567, AL079658, NM_002776, BE261944, NM_006379, AI002238, X81789, NM_002122,

AB001914, AA311919, AI381750, AA292998, BE439580, AI677897, N72403, BE003054, AL035588, AI080491, AW770994, H24177, AF146761, NM_001955, AI680737, AI752666, AA505445, BE246649, and NM_003955; and

- (v) a sequence that is complementary to any one of the sequences set forth in (i) or (ii) or (iii) or (iv).

45. The method of claim 44 wherein the nucleic acid probe comprises a sequence selected from the group consisting of:

- (i) a sequence comprising at least about 20 contiguous nucleotides from a sequence selected from the group consisting of SEQ ID NOs: 63, 65, 67, 69, 71, and 73;
- (ii) a sequence that hybridizes under at least low stringency hybridization conditions to at least about 20 contiguous nucleotides from a sequence selected from the group consisting of SEQ ID NOs: 63, 65, 67, 69, 71, 73, 75, 77, 79, 81 and 83;
- (iii) a sequence that is at least about 80% identical to a sequence selected from the group consisting of SEQ ID NOs: 63, 65, 67, 69, 71, 73, 75, 77, 79, 81 and 83;
- (iv) a sequence that encodes an amino acid sequence selected from the group consisting of SEQ ID NOs: 64, 66, 68, 70, 72, 74, 76, 78, 80, 82 and 84; and
- (v) a sequence that is complementary to (i) or (ii) or (iii) or (iv).

46. A method of determining the likelihood of survival of a subject suffering from an ovarian cancer, said method comprising contacting a biological sample from said subject being tested with an antibody for a time and under conditions sufficient for an antigen-antibody complex to form and then detecting the complex wherein an enhanced level of the antigen-antibody complex for the subject being tested compared to the amount of the antigen-antibody complex formed for a control subject not having ovarian cancer indicates that the subject being tested has a poor probability of survival, and wherein said antibody binds to a polypeptide comprising an amino acid sequence comprising at least about 10 contiguous amino acid residues of a sequence encoded by a nucleic acid set forth in Table 1 and having an Accession Number selected from the group consisting of: NM_003014, AA046217, NM_015902, T83882, AB040888, AA628980, AI623351, AW614420, AA243499, AF251237, AI970797, AF145713, X78565, T97307, BE243845, AW068302, AL133561, BE313555, X07820, AI973016, AF084545, U41518, Z11894, AW138190, BE086548, W47196, AI796870, X02761, AW968613, AW972565, AF045229, AW953853, U52426, F06700, AI798863, H52761, BE546947, AU076643, U20536, AA581602, AJ245210, X65965, AI806770, BE386490, AW581992, U77534, AL034417, L10343, AW518944, W28729, AI640160, U11862, AW295980, X59135,

BE466173, AI354722, M90464, AA829286, AI333771, BE465867, NM_014992, BE616902, AA430373, R27430, BE387335, AW264102, AW952323, AA088177, BE614567, AL079658, NM_002776, BE261944, NM_006379, AI002238, X81789, NM_002122, AB001914, AA311919, AI381750, AA292998, BE439580, AI677897, N72403, BE003054, AL035588, AI080491, AW770994, H24177, AF146761, NM_001955, AI680737, AI752666, AA505445, BE246649, and NM_003955.

47. The method of claim 46 wherein the antibody binds to a polypeptide comprising an amino acid sequence comprising at least about 10 contiguous amino acid residues of a sequence having at least about 80% identity to a sequence selected from the group consisting of SEQ ID NOs: 64, 66, 68, 70, 72, 74, 76, 78, 80, 82 and 84.

48. A method of determining the likelihood of survival of a subject suffering from a serous ovarian cancer, said method comprising contacting a biological sample from said subject being tested with a nucleic acid probe for a time and under conditions sufficient for hybridization to occur and then detecting the hybridization wherein an elevated level of hybridization of the probe for the subject being tested compared to the hybridization obtained for a control subject not having ovarian cancer indicates that the subject being tested has a poor probability of survival, and wherein said nucleic acid probe comprises a sequence selected from the group consisting of:

- (i) a sequence comprising at least about 20 contiguous nucleotides from a nucleic acid comprising the nucleotide sequence set forth in SEQ ID NO: 71 or 73;
- (ii) a sequence that hybridizes under at least low stringency hybridization conditions to at least about 20 contiguous nucleotides from a nucleic acid comprising the nucleotide sequence set forth in SEQ ID NO: 71 or 73;
- (iii) a sequence that is at least about 80% identical to (i) or (ii) and encoding an sFRP protein or a SOCS3 protein;
- (iv) a sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 72 or 74; and
- (v) a sequence that is complementary to any one of the sequences set forth in (i) or (ii) or (iii) or (iv).

49. A method of determining the likelihood of survival of a subject suffering from a serous ovarian cancer, said method comprising contacting a biological sample from said subject being tested with an antibody for a time and under conditions sufficient for an antigen-antibody complex to form and then detecting the complex wherein an enhanced

level of the antigen-antibody complex for the subject being tested compared to the amount of the antigen-antibody complex formed for a control subject not having ovarian cancer indicates that the subject being tested has a poor probability of survival, and wherein said antibody binds to an sFRP polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 72 or a SOCS3 polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 74.

50. A method of determining the likelihood of survival of a subject suffering from a serous ovarian cancer, said method comprising contacting a biological sample from said subject being tested with at least two antibodies for a time and under conditions sufficient for antigen-antibody complexes to form and then detecting the complexes wherein an enhanced level of the antigen-antibody complexes for the subject being tested compared to the amount of the antigen-antibody complexes formed for a control subject not having ovarian cancer indicates that the subject being tested has a poor probability of survival, and wherein one antibody binds to an sFRP polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 72 and wherein one antibody binds to a SOCS3 polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 74.

51. The method according to any one of claims 44 to 47 wherein the ovarian cancer is an epithelial ovarian cancer.

52. The method according to any one of claims 44 to 47 wherein the ovarian cancer is selected from the group consisting of serous ovarian cancer, non-invasive ovarian cancer, mixed phenotype ovarian cancer, mucinous ovarian cancer, endometrioid ovarian cancer, clear cell ovarian cancer, papillary serous ovarian cancer, Brenner cell and undifferentiated adenocarcinoma.

53. The method according to claim 52 wherein the ovarian cancer is selected from the group consisting of serous ovarian cancer, mucinous ovarian cancer, endometrioid ovarian cancer and clear cell ovarian cancer.

54. A method of determining the likelihood that a subject will suffer from a recurrence of an ovarian cancer, said method comprising contacting a biological sample from said subject being tested with a nucleic acid probe for a time and under conditions sufficient for hybridization to occur and then detecting the hybridization wherein an elevated level of hybridization of the probe for the subject being tested compared to the hybridization

obtained for a control subject not having ovarian cancer indicates that the subject being tested has a high probability of recurrence, and wherein said nucleic acid probe comprises a sequence selected from the group consisting of:

- (i) a sequence comprising at least about 20 contiguous nucleotides from a nucleic acid set forth in Table 1 and having an Accession Number selected from the group consisting of: M86849, AW963419, BE298665, AK000637, BE077546, T97307, R24601, BE090176, AA393907, W28729, BE313754, AW673081, AA356694, L08239, BE397649, NM_012317, NM_000947, AJ250562, AL040183, BE207573, BE564162, BE439580, AW067800, AA569756, AW138190, AF126245, L10343, NM_002514, AI863735, NM_005397, W26391, H15474, U51166, AA243499, AW408807, AI738719, AB040888, BE313077, AI677897, C14898, AI821730, AF007393, H65423, N46243, AA095971, U20350, NM_005756, D19589, AW957446, AW294647, BE159718, AI888490, AA022569, BE147740, AI798863, BE464341, AL080235, AI557212, X75208, AA628980, BE242587, NM_005512, AW953853, AU076611, AW968613, AL353944, BE614149, AA292998, H12912, AA188763, AK000596, AI970797, AW519204, Z42387, AF145713, AA972412, AK001564, AW959861, BE313555, W25005, AI193356, AF111106, AI130740, AA985190, BE221880, AF084545, R26584, AW247380, AA364261, U25849, AF262992, AW342140, AL133572, AI497778, AI745379, U51712, AW375974, AF251237, NM_000636, AA130986, AA216363, AA628980, AA811657, AA897108, AB040888, AF212225, AI089575, AI282028, AI368826, AI718702, AI827248, AK002039, AL109791, AW090198, AW296454, AW445034, AW452948, AW470411, AW885727, AW970859, AW979189, BE165866, BE175582, BE242587, BE271927, BE439580, BE464016, D63216, F34856, M83822, N33937, N49068, N51357, N80486, NM_000954, NM_005756, NM_016652, R26584, R31178, W05391, W25005, W45393, W68815, X65965, X76732 and Z45051,
- (ii) a sequence that hybridizes under at least low stringency hybridization conditions to at least about 20 contiguous nucleotides from a nucleic acid set forth in Table 1 and having an Accession Number selected from the group consisting of: M86849, AW963419, BE298665, AK000637, BE077546, T97307, R24601, BE090176, AA393907, W28729, BE313754, AW673081, AA356694, L08239, BE397649, NM_012317, NM_000947, AJ250562, AL040183, BE207573, BE564162, BE439580, AW067800, AA569756, AW138190, AF126245, L10343, NM_002514, AI863735, NM_005397, W26391, H15474, U51166, AA243499, AW408807, AI738719, AB040888, BE313077, AI677897, C14898, AI821730, AF007393,

H65423, N46243, AA095971, U20350, NM_005756, D19589, AW957446, AW294647, BE159718, AI888490, AA022569, BE147740, AI798863, BE464341, AL080235, AI557212, X75208, AA628980, BE242587, NM_005512, AW953853, AU076611, AW968613, AL353944, BE614149, AA292998, H12912, AA188763, AK000596, AI970797, AW519204, Z42387, AF145713, AA972412, AK001564, AW959861, BE313555, W25005, AI193356, AF111106, AI130740, AA985190, BE221880, AF084545, R26584, AW247380, AA364261, U25849, AF262992, AW342140, AL133572, AI497778, AI745379, U51712, AW375974, AF251237, NM_000636, AA130986, AA216363, AA628980, AA811657, AA897108, AB040888, AF212225, AI089575, AI282028, AI368826, AI718702, AI827248, AK002039, AL109791, AW090198, AW296454, AW445034, AW452948, AW470411, AW885727, AW970859, AW979189, BE165866, BE175582, BE242587, BE271927, BE439580, BE464016, D63216, F34856, M83822, N33937, N49068, N51357, N80486, NM_000954, NM_005756, NM_016652, R26584, R31178, W05391, W25005, W45393, W68815, X65965, X76732 and Z45051;

(iii) a sequence that is at least about 80% identical to (i) or (ii);

(iv) a sequence that encodes a polypeptide encoded by a nucleic acid set forth in Table 1 and having an Accession Number selected from the group consisting of: M86849, AW963419, BE298665, AK000637, BE077546, T97307, R24601, BE090176, AA393907, W28729, BE313754, AW673081, AA356694, L08239, BE397649, NM_012317, NM_000947, AJ250562, AL040183, BE207573, BE564162, BE439580, AW067800, AA569756, AW138190, AF126245, L10343, NM_002514, AI863735, NM_005397, W26391, H15474, U51166, AA243499, AW408807, AI738719, AB040888, BE313077, AI677897, C14898, AI821730, AF007393, H65423, N46243, AA095971, U20350, NM_005756, D19589, AW957446, AW294647, BE159718, AI888490, AA022569, BE147740, AI798863, BE464341, AL080235, AI557212, X75208, AA628980, BE242587, NM_005512, AW953853, AU076611, AW968613, AL353944, BE614149, AA292998, H12912, AA188763, AK000596, AI970797, AW519204, Z42387, AF145713, AA972412, AK001564, AW959861, BE313555, W25005, AI193356, AF111106, AI130740, AA985190, BE221880, AF084545, R26584, AW247380, AA364261, U25849, AF262992, AW342140, AL133572, AI497778, AI745379, U51712, AW375974, AF251237, NM_000636, AA130986, AA216363, AA628980, AA811657, AA897108, AB040888, AF212225, AI089575, AI282028, AI368826, AI718702, AI827248, AK002039, AL109791, AW090198, AW296454, AW445034,

AW452948, AW470411, AW885727, AW970859, AW979189, BE165866, BE175582, BE242587, BE271927, BE439580, BE464016, D63216, F34856, M83822, N33937, N49068, N51357, N80486, NM_000954, NM_005756, NM_016652, R26584, R31178, W05391, W25005, W45393, W68815, X65965, X76732 and Z45051; and

- (v) a sequence that is complementary to any one of the sequences set forth in (i) or (ii) or (iii) or (iv).

55. The method of claim 54 determining the likelihood that a subject will suffer from a recurrence of an ovarian cancer, said method comprising contacting a biological sample from said subject being tested with an antibody for a time and under conditions sufficient for an antigen-antibody complex to form and then detecting the complex wherein an enhanced level of the antigen-antibody complex for the subject being tested compared to the amount of the antigen-antibody complex formed for a control subject not having ovarian cancer indicates that the subject being tested has a high probability of recurrence, and wherein said antibody binds to a polypeptide comprising an amino acid sequence comprising at least about 10 contiguous amino acid residues of a sequence encoded by a nucleic acid set forth in Table 1 and having an Accession Number selected from the group consisting of: M86849, AW963419, BE298665, AK000637, BE077546, T97307, R24601, BE090176, AA393907, W28729, BE313754, AW673081, AA356694, L08239, BE397649, NM_012317, NM_000947, AJ250562, AL040183, BE207573, BE564162, BE439580, AW067800, AA569756, AW138190, AF126245, L10343, NM_002514, AI863735, NM_005397, W26391, H15474, U51166, AA243499, AW408807, AI738719, AB040888, BE313077, AI677897, C14898, AI821730, AF007393, H65423, N46243, AA095971, U20350, NM_005756, D19589, AW957446, AW294647, BE159718, AI888490, AA022569, BE147740, AI798863, BE464341, AL080235, AI557212, X75208, AA628980, BE242587, NM_005512, AW953853, AU076611, AW968613, AL353944, BE614149, AA292998, H12912, AA188763, AK000596, AI970797, AW519204, Z42387, AF145713, AA972412, AK001564, AW959861, BE313555, W25005, AI193356, AF111106, AI130740, AA985190, BE221880, AF084545, R26584, AW247380, AA364261, U25849, AF262992, AW342140, AL133572, AI497778, AI745379, U51712, AW375974, AF251237, NM_000636, AA130986, AA216363, AA628980, AA811657, AA897108, AB040888, AF212225, AI089575, AI282028, AI368826, AI718702, AI827248, AK002039, AL109791, AW090198, AW296454, AW445034, AW452948, AW470411, AW885727, AW970859, AW979189, BE165866, BE175582, BE242587, BE271927, BE439580,

BE464016, D63216, F34856, M83822, N33937, N49068, N51357, N80486, NM_000954, NM_005756, NM_016652, R26584, R31178, W05391, W25005, W45393, W68815, X65965, X76732 and Z45051.

5 56. The method according to claim 54 or 55 wherein the ovarian cancer is an epithelial ovarian cancer.

57. The method according to any one of claims 54 to 56 wherein the ovarian cancer is selected from the group consisting of serous ovarian cancer, non-invasive ovarian
10 cancer, mixed phenotype ovarian cancer, mucinous ovarian cancer, endometrioid ovarian cancer, clear cell ovarian cancer, papillary serous ovarian cancer, Brenner cell and undifferentiated adenocarcinoma.

58. The method according to claim 57 wherein the ovarian cancer is selected from the
15 group consisting of serous ovarian cancer, mucinous ovarian cancer, endometrioid ovarian cancer and clear cell ovarian cancer.

59. The method according to any one of claims 35 to 58 wherein the biological sample is contacted with a plurality of nucleic acid probes and/or antibodies and/or polypeptides.
20

60. A method for identifying a compound that modulates an ovarian cancer-associated polypeptide, the method comprising :

- (i) contacting the compound with a ovarian cancer-associated polypeptide, the polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence
25 at least 80% identical to a sequence as shown in Tables 1-3; and
(ii) determining the functional effect of the compound upon the polypeptide.

61. A method for determining a candidate compound for the treatment of ovarian cancer comprising :

- (i) administering a test compound to a mammal having ovarian cancer or a cell
30 isolated therefrom;
(ii) comparing the level of gene expression of a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-3 in a treated cell or mammal with the level of gene expression of the
35 polynucleotide in a control cell or mammal, wherein a test compound that

modulates the level of expression of the polynucleotide is a candidate for the treatment of ovarian cancer.

62. An assay device for use in the diagnosis or prognosis of ovarian cancer, said device comprising a plurality of polynucleotides immobilized to a solid phase, wherein each of said polynucleotides consists of a gene as listed in any one of Tables 1-3.

63. The device of claim 62 consisting of a substantially planar chip.

64. An assay device for use in the diagnosis or prognosis of ovarian cancer, said device comprising a plurality of different antibodies immobilized to a solid phase, wherein each of said antibodies binds to a polypeptide listed in Tables 1-3.

65. The device of claim 64 consisting of a substantially planar chip.

66. Use of a polynucleotide as set forth in any one of Tables 1-3 in the diagnosis or prognosis of ovarian cancer or for the preparation of a medicament for the treatment of ovarian cancer.

67. Use of a vector comprising a polynucleotide as set forth in any one of Tables 1-3 in the diagnosis or prognosis of ovarian cancer or for the preparation of a medicament for the treatment of ovarian cancer.

68. Use of an isolated polypeptide as set forth in any one of Tables 1-3 in the diagnosis or prognosis of ovarian cancer or for the preparation of a medicament for the treatment of ovarian cancer.

69. Use of an antibody that binds to an isolated polypeptide as set forth in any one of Tables 1-3 in the diagnosis or prognosis of ovarian cancer or for the preparation of a medicament for the treatment of ovarian cancer.

70. A method of diagnosing an ovarian cancer in a human or animal subject being tested said method comprising determining aberrant methylation in a promoter sequence that regulates expression of a tumor suppressor gene in a biological sample from said subject compared to the methylation of the promoter in nucleic acid obtained for a control

subject not having ovarian cancer wherein said aberrant methylation indicates that the subject being tested has an ovarian ovarian cancer.

5 71. The method of claim 70 wherein hypermethylation of the promoter sequence is determined.

72. The method of claim 70 or 71 wherein the methylation is determined in the promoter region that regulates expression of an MCC gene comprising a sequence selected from the group consisting of:

- 10 (i) the nucleotide sequence set forth as SEQ ID NO: 3;
- (ii) a sequence that hybridizes under at least low stringency hybridization conditions to the nucleotide sequence set forth as SEQ ID NO: 3;
- (iii) a sequence that is at least about 80% identical to (i) or (ii);
- (iv) a sequence that encodes a polypeptide encoded by a nucleotide sequence set
15 forth as SEQ ID NO: 3; and
- (v) a sequence that is complementary to any one of the sequences set forth in (i) or (ii) or (iii) or (iv).

20 73. The method according to any one of claims 70 to 72 wherein the ovarian cancer that is diagnosed is an epithelial ovarian cancer.